a a region that doesn't interact with clone
   10 (NMP1), 9 and 15 in the 2-hybrid test

b a region that interact with these clones
   as strongly as the full-size TRAF2

☒ - RING finger motif

☐ - TFIIIA-like zinc-finger motifs

☒ - N-TRAF

☒ - C-TRAF

Fig. 1
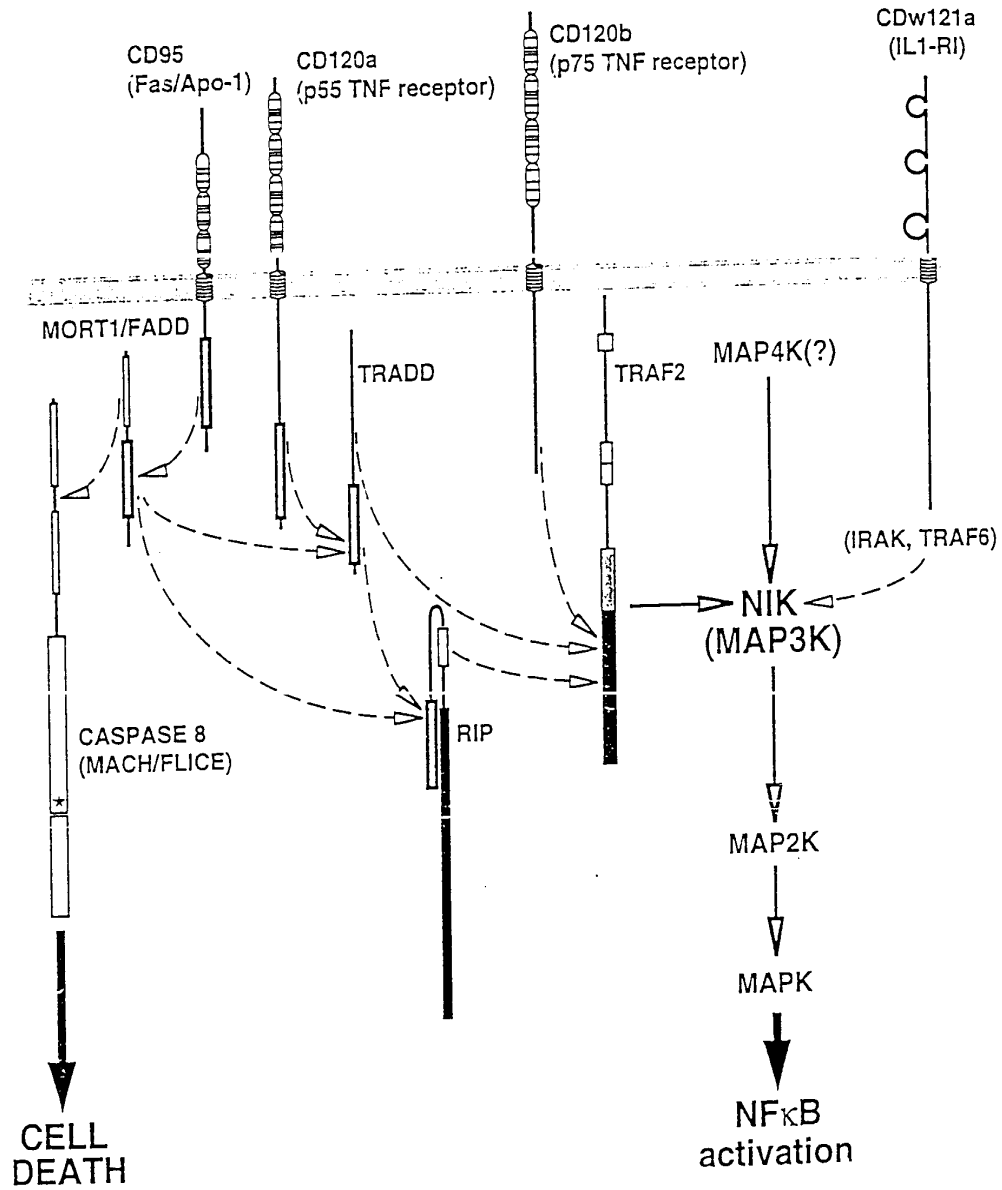
Fig. 2

New Kinase Sequences

A. Amino Acid sequence: boxed - kinase domain, underlined - CARD domain.

```
                  10         20         30         40         50         60         70         80         90        100
  1 MNGEAICSAL PTIPYHKLAD LRYLSRGASG TVSSARHADW RVQVAVKHLH IHTPLLDSER KDVLREAEIL HKARFSYIFP ILGICNEPEF LGIVTEYMPR 100
101 GSLNELLHRK TEYPDVAWPL RFRILHEIAL GVNYLHNMTP PLLHHDLKTQ NILLDNEFHV KIADFGLSKW RMMSLSQSFS SKSAPEGGTI IYMPPENYEP 200
201 GQKSRASIKH DIYSYAVITW EVLSRKQPFE DVTNPLQIMY SVSQGHRPVI NEESLPYDIP HRARMISLIE SGWAQNPDER PSFLKCLIEL EPVLRTFEEI 300
301 TFLEAVIQLK KTKLQSVSSA IHLCDKKKME LSLNIPVNIG PQEESCGSSQ LHENSGSPET SRSLPAPQDN DFLSRKAQIC YFMKLHHCPG NHSWDSTISG 400
401 SQRAAFCDHK TTPCSSAIIN PLSTAGNSER LQPGIAQQWI QSKREHIVNQ MTEACLNQSL DALLSRDLIM KEDYELVSTK PTRTSKVRQL LDTTDIQGEE 500
501 FAKVIVQKLK DNKQMGLQPY PEILVVSRSP SLNLLQNKSM 540
                  10         20         30         40         50         60         70         80         90        100
```

B. Nucleotide sequence.

```
                10         20         30         40         50         60         70         80         90        100
   1 GGCCATTATG GATGGATGGG CGGGGCTACG GCGTTGGCAC CAGTCTCTAG AAAGAAGTC  AGCTCTTGTT CGGAGAAGCA GCGGCTGGCG TGGGCCATCC 100
 101 GGGGAATGGG CGCCCTCGTG ACCTAGTGTT GCGGGGCAAA AAGGGTCTTG CCGGCCTCGC TCGTGCAGGG GCGTATCTGG GCGCCGTGGG 200
 201 AGCCTTGGGA GCCGCCGCAG CAGGGGCAC  ACCCGGAACC GGCCTGAGCG CCCGGACCA  TGAACGGGGA GCCCATCTGC AGCGCCCTGC CCACCATTCC 300
 301 CTACCACAAA CTCGCCGACC TGCGCTACCT GAGCCGCGGC GCCTCTGGCA CTGTCGCGTC CGCCCGCCAC GCAGACTGGC GCTCCAGT   GGCCGTGAAG 400
 401 CACCTGCACA TCCACACTCC GCTGCTCGAC AGTGAAAGAA AGGATGTTT  AAGAGAAGCT GAAATTTAC  ACAAAGCTAG ATTAGTTAC  ATTTTTCCAA 500
 501 TTTTGGGAAT TTGCAACACG CCTGAATTT  TGGGAATAGT TACTCAATAC ATGCCAAATG GATCATTAAA TGAACTCCTA CATAGGAAAA CTGAATATCC 600
 601 TGATGTTGCT TGGCCATTGA GATTTCGCAT CCTGCATGAA ATTGCCCTTG GTGTAAATTA CCTGCACAAT ATGACTCCTC CTTACTTCA  TCATGACTTG 700
 701 AAGACTCAGA ATATCTTATT GGACAATGAA TTTCATCTTA AGATTGCAGA TTTTGGTTTA TCAAAGTGGC GCATGATGTC CCTCTCACAG TCACGAAGTA 800
 801 GCAAATCTGC ACCAGAAGGA GGACAATTA  TTTATATGCC AAGGGCCAGT ATCAAGCACG ATATATAG 900
 901 CTATGCAGTT ATCACATGGG AAGTGTTATC CAGAAAACAG CCTTTTGAAG ATGTCACCAA TCCTTTGCAG ATAATGTATA GTGTGTCACA AGGACATCGA 1000
1001 CCTGTTATTA ATGAAGAAAG TTTGCCATAT GATATACCTC ACCGAGCACG TATGATCTCT CTAATAGAAA GTGGATGGGC ACAAAATCCA GATGAAAGTT 1100
1101 CATCTTTCTT AAAATGTTTA ATAGAACTTG AACCAGTTTT GAGAACATTT GAAGAGATAA CTTTTCTTGA AGCTGTTATT CACCTAAAGA AAACAAAGTT 1200
1201 ACAGAGTGTT TCAAGTGCCA TTCACCTATG TGACAAGAAG AAAATGGAAT TATCTCTGAA CATACCTGTA AATCATGGTC CAGAGGAATC AGCAGGTCAA 1300
1301 TCCTCTCAGC TCCATGAAAA TAGTGGTTCT CCTGAAACTT CAAGGTCCCT GCCAGCTCCT CAAGATAATG ATTTTCTGTC TAGAAAGCT  CAAGAACTGG 1400
1401 ATTTTATGAA GCTGCATCAC CACTCTCCAG GGAAATCGAC TGCATTCTGT GATCACAAGA CCACTCCATG TTCCAGCATT 1500
1501 CTCTTCAGCA ATAATAAATC AGCCCCTTCT GTCCAGGGAC TTGATCATGA GGAAGAATT  GCTCCAAAGT TATAGTACAA AAAATGGAAG GGAAGACATT 1600
1601 GTGAACCAAA TGACAGAAGC CTGCCTTAAC CAGTCGCTAG AGGAAGAAT  TGCCAAAGT  TATAGTACAA AATTGAAAG  ATAACAAACA 1700
1701 CTACAAGGAC CTCAAAAGTC AGACAATTAC TAGACACTAC TGACATCCAA CTTTAAATTT ACTTCAAAAT AAAAGCATGT AAATGACTGT TTTTCAGAA 1800
1801 AATGGGTCTT CAGCCTTACC CGGAAATACT TGTGGTTTCT AGATCACCAT TTTATATAAA TCCGTGAGTA TTAAAGCTTW AWHRAARGKT CTTTSRKTAA 1900
1901 GAAATGTGTT TCATAAAAGG ATATTTATAT CTCTGTTTGC TTGAGCTTTT TTATATACAG TAAAAGCTTG AATTTGAAAA 2000
2001 ATATTAGTCT CCCTCCATGA CACTGCAGTA TTTTTTTTAA TTAMTACAAG TAAAAGCTTG AATTTGAAAA AAAAAAA AAAAAAAA A 2098
                10         20         30         40         50         60         70         80         90        100
```

Fig. 3

NORTHERN BLOT ANALYSIS OF B1 mRNA EXPRESSION

Fig. 4

KINASE DOMAIN   CARD DOMAIN

	NF-kB	Cell death potentiation	JNK
B1	+++	+++	+++
B1mut	+++	+++	+++
Δ CARD	-	+	NT
Δ Xba	-	-	NT
Δ Bam	-	-	NT
Δ Nde	+	+	NT
Δ K	+	+	+

B1mut: 47K→A

ΔCARD: 454
ΔXba: 374
ΔBam: 347
ΔNde: 244
ΔK: 315
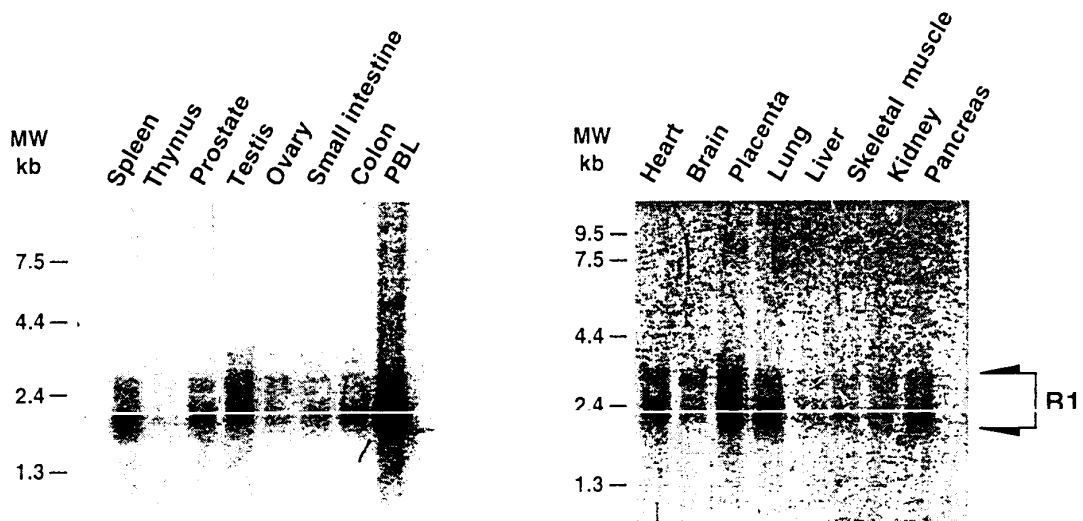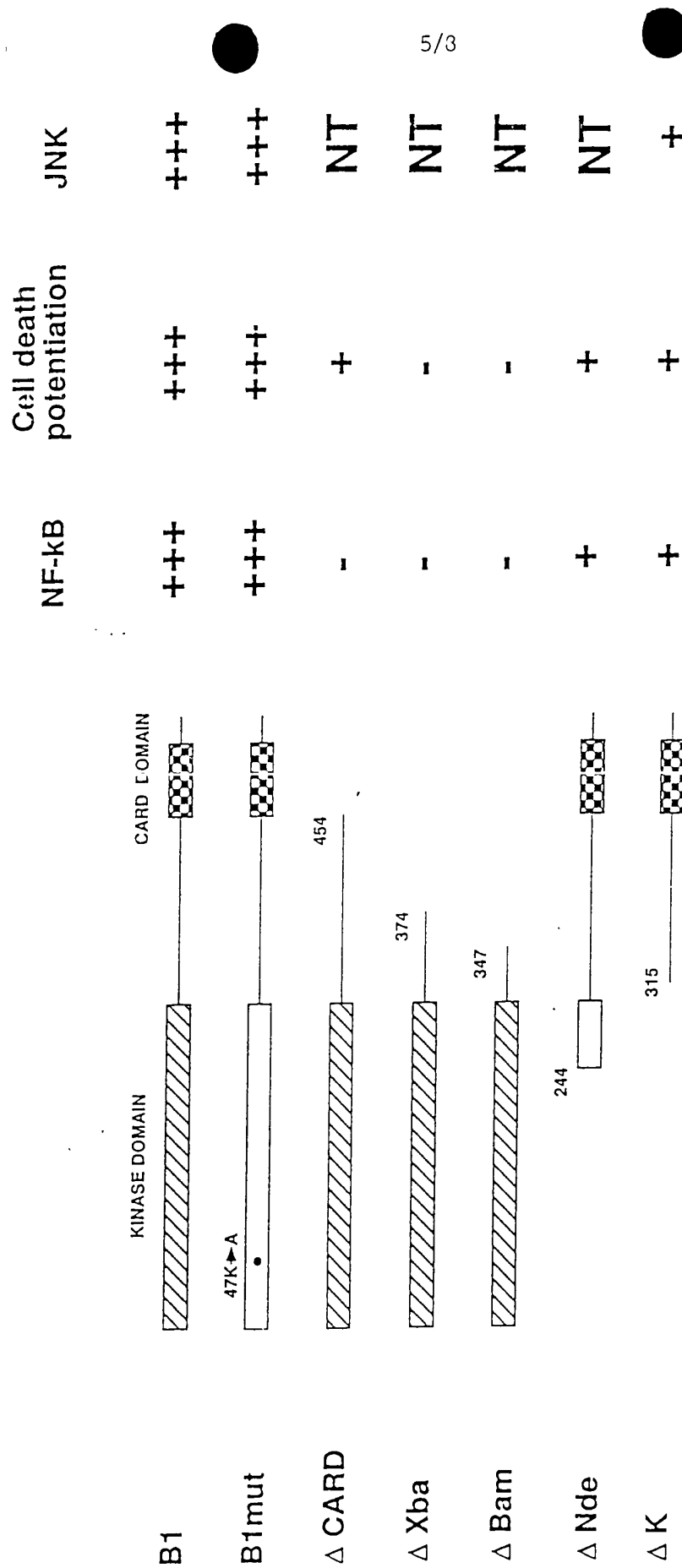
Fig. 5

Deletion analysis of B1 ability
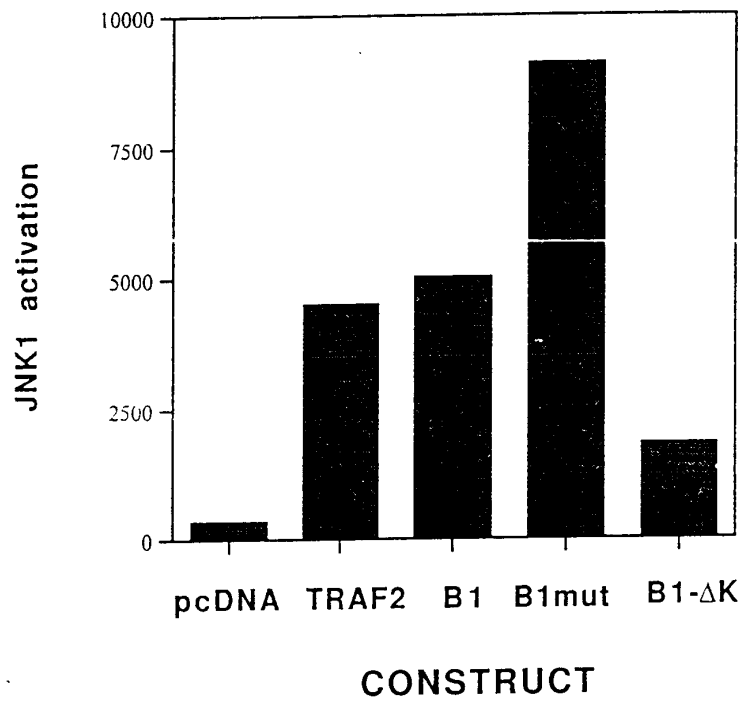## to activate NF-kB transcriptional factor
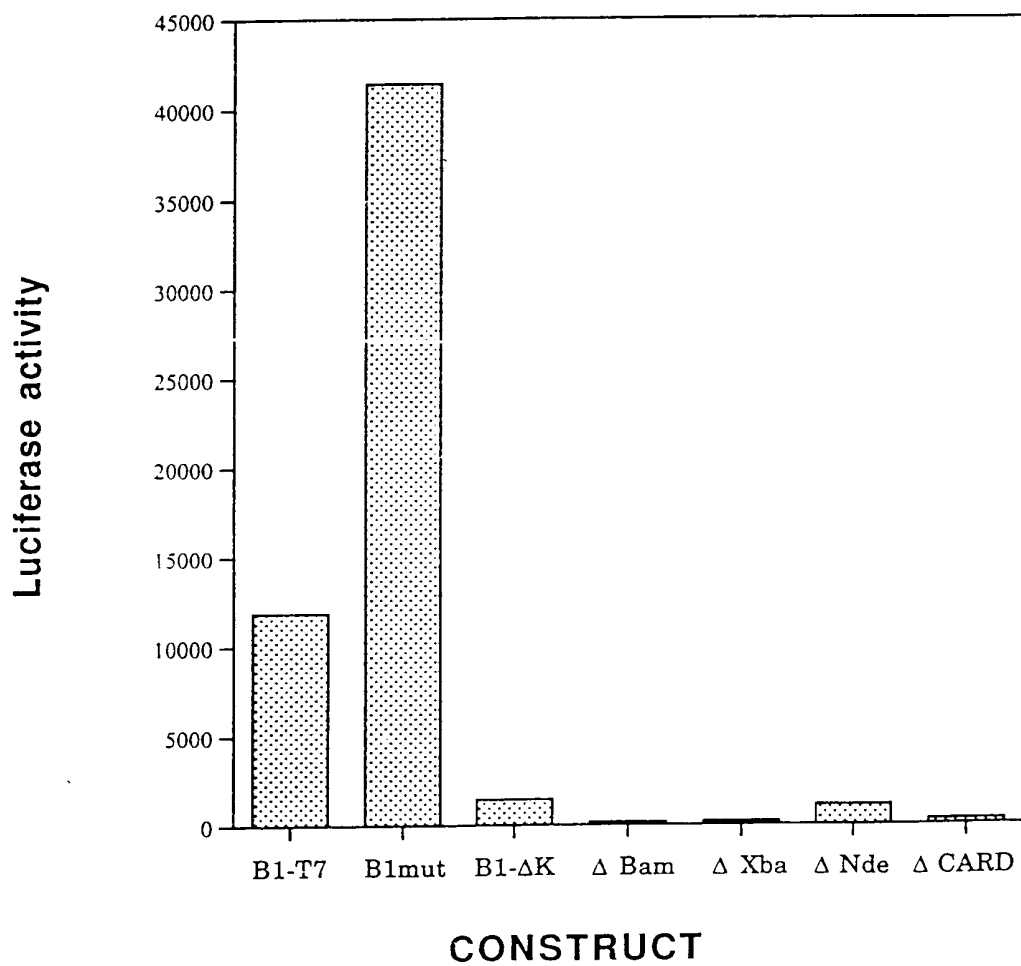
Fig. 6

Mutational analysis of B1 ability to activate JNK1 pathway
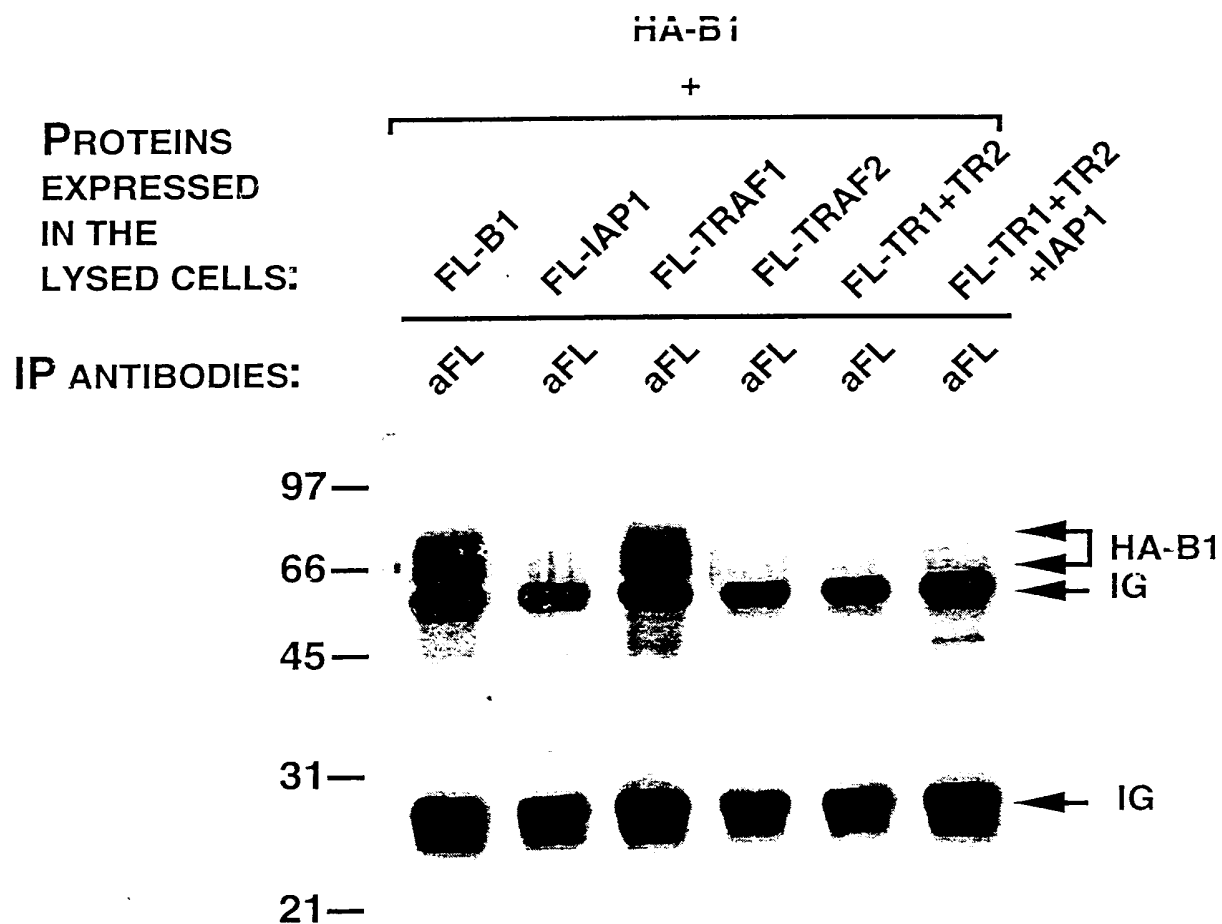

Fig. 7

B1 interacts with TRAF1 in vivo

Fig. 8